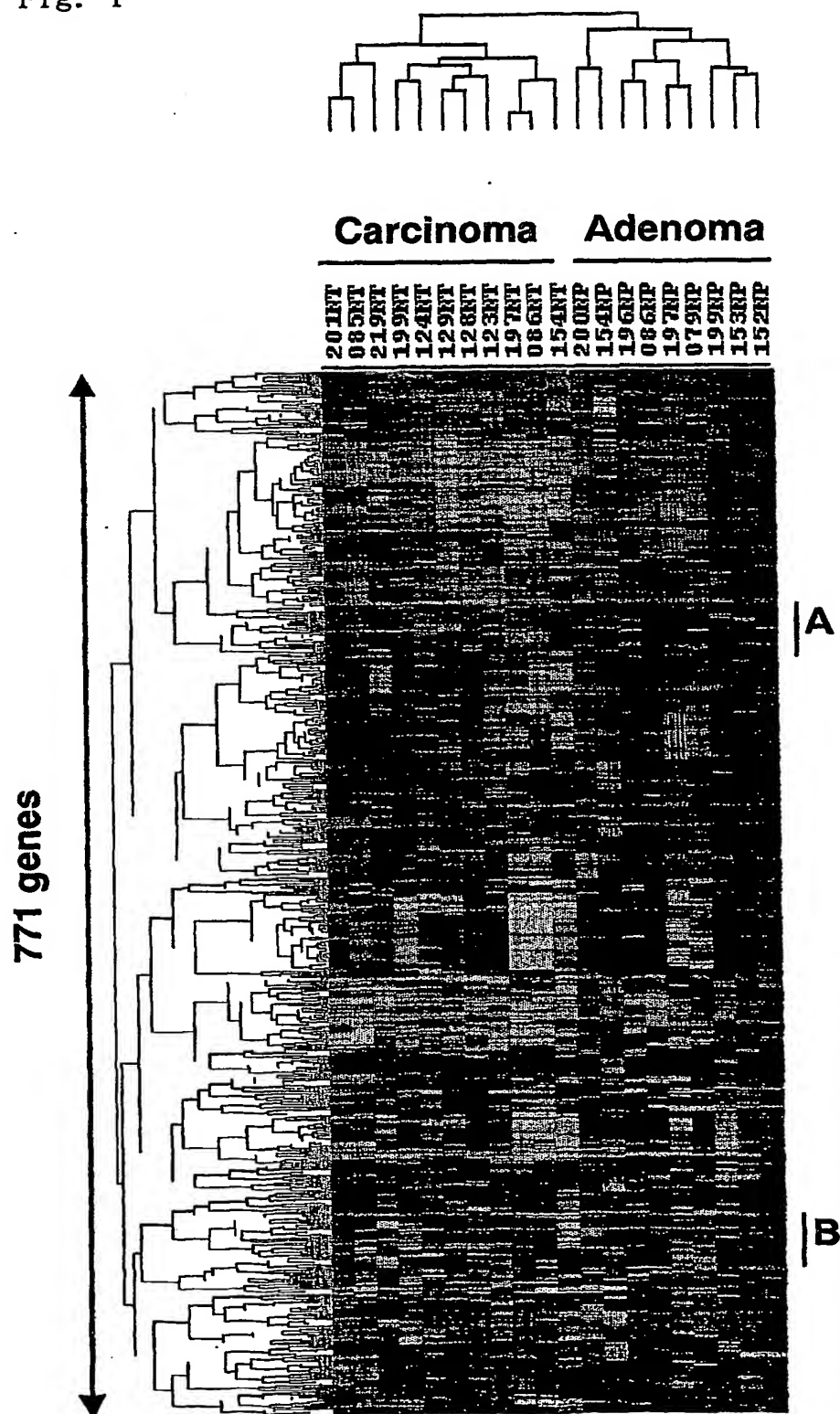


1 / 6

Fig. 1



2 / 6

Fig. 2

Accession No.	Gene	Description	Function	(G3/G6)ave	(G3/G6)2, % (n=20)
U08002	TCFBI	transforming growth factor, beta-induced, 68kD	cell adhesion/cytoskeleton	12.96	100
U08003	TCFBI	transforming growth factor, beta-induced, 68kD	cell adhesion/cytoskeleton	12.89	95
U08004	ITIM2	interferon induced transmembrane protein 2 (I-40)	immune response	5.26	95
U08005	CD81	CD81 antigen (target of antiproliferative antibody 1)	signal transduction	4.34	95
U08006	LAP18	leukemia-associated phosphoprotein p18 (statmin)	signal transduction	6.27	95
U08007	CT77	cleaverin containing TCF1, subunit 7 (eta)	RNA/protein processing	3.47	90
U08008	HSPCB	heat shock 90D protein 1, beta	RNA/protein processing	2.66	90
U08009	PABPC1	poly(A)-binding protein, cytoplasmic 1	RNA/protein processing	3.23	90
U08010	RPL20	ribosomal protein L20	RNA/protein processing	4.1	90
U08011	MAC149559	macrophage myristoylated alanine-rich G-kinase substrate	signal transduction	4.31	90
U08012	FLJ20315	hypothetical protein FLJ20315	unknown	4.43	90
U08013	RPS3	ribosomal protein S3	RNA/protein processing	5.21	85
U08014	RPSAX	ribosomal protein S4, X-linked	RNA/protein processing	4.6	85
U08015	HECH	heterochronin-like protein 1	unknown	4.02	85
U08016	RAN	RAN, member RAS oncogene family	cell cycle	3.36	80
U08017	RAN	RAN, member RAS oncogene family	cell cycle	3.24	80
U08018	HMGY	high-mobility group (nucleosome chromosomal) protein isoforms 1 and Y	oncogene	4.02	80
U08019	HSPCB	heat shock 90D protein 1, beta	RNA/protein processing	3.17	80
U08020	HSPCB	heat shock 90D protein 1, beta	RNA/protein processing	3.45	80
U08021	MRPL3	mitochondrial ribosomal protein L3	RNA/protein processing	2.93	80
U08022	PABPC1	poly(A)-binding protein, cytoplasmic 1	RNA/protein processing	2.86	80

2 / 1 / 6

S9263	RPS3	ribosomal protein S3	RNA/protein processing	4.22	80
EP02628		cDNA coding for human polypeptide chain elongation factor-1 alpha	RNA/protein processing	3.2	80
DS374	HUG1	high-mobility group (nonhistone chromosomal) protein 1	transcription regulation	3.23	80
Y00711	LHB	lactate dehydrogenase B	tumor associated	6.47	80
A076603	ESTs	ESTs	unknown	3.12	80
H16580	ODC1	ornithine decarboxylase 1	cell growth	3.9	75
L17131	HUGY	high-mobility group (nonhistone chromosomal) protein isoforms 1 and Y	oncogene	4.08	75
AA705503	EEF1A1	eukaryotic translation elongation factor 1 alpha 1	RNA/protein processing	3.12	75
R61287	EF3S6	eukaryotic translation initiation factor 3, subunit 6 (40kD)	RNA/protein processing	3.26	75
U62932	EF3S6	eukaryotic translation initiation factor 3, subunit 6 (40kD)	RNA/protein processing	3.82	75
H16560	HSP9B	heat shock 90kD protein 1, beta	RNA/protein processing	3.1	75
M22382	HSPD1	heat shock 60kD protein 1 (chaperonin)	RNA/protein processing	4.6	75
A087287	NOL42	nucleolar protein family A, member 2 (H/ACA small nuclear RNP-s)	RNA/protein processing	3	75
S7822	RPS27A	ribosomal protein S27a	RNA/protein processing	2.6	75
AA083204	RPS3	ribosomal protein S3	RNA/protein processing	2.74	75
A000002	CCNI	cyclin I	unknown	2.96	75
R12013	HDCN3AP	hypothetical protein HDCN3AP	unknown	3.33	75
L06132	VDAC1	voltage-dependent anion channel 1	bioenergetics	2.77	70
U66818	UBE2I	ubiquitin-conjugating enzyme E2 (homologous to yeast UBC9)	cell cycle	3.19	70
L04208	IMPDH2	IMP (inosine triphosphate) dehydrogenase 2	cell growth	2.91	70

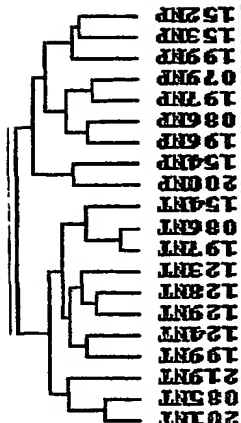
Fig. 2/1

2 / 2 / 6

D58184	IDEK	IDEK oncogene (DNA binding)	oncogene	315	70
A467655	NPY1	nucleophosmin (nuclear phosphoprotein B23, numatrin)	oncogene	503	70
D17554	RPL6	ribosomal protein L6	RNA/protein processing	346	70
U08953	RPL9	ribosomal protein L9	RNA/protein processing	37	70
U17224	RPS3A	ribosomal protein S3A	RNA/protein processing	325	70
A491688	BRF1	bradykinin response factor 1 (EGR-response factor 1)	signal transduction	281	70
A471494	HMG2	high-mobility group (nonhistone chromosomal) protein 2	transcription regulation	454	70
A457959	CYP2S1	cytochrome P450 family member predicted from ESTs	unknown	403	70
A582493	EST	EST	unknown	328	70
U03629	CD13	cadherin 3, type 1, P-cadherin (placental)	cell adhesion/cytoskeleton	359	65
A463400	HNRPA1	heterogeneous nuclear ribonucleoprotein A1	RNA/protein processing	372	65
X17205	RPS2	ribosomal protein S2	RNA/protein processing	396	65
K00558	K-ALPHA	tubulin, alpha, ubiquitous	cell adhesion/cytoskeleton	305	60
D07665	HSPCA	heat shock 90D protein 1, alpha	RNA/protein processing	237	60
D14531	RPL9	ribosomal protein L9	RNA/protein processing	299	60
U03079	PLAB	prostate differentiation factor	signal transduction	75	60
L15533	PAP	pancreatitis-associated protein	cell adhesion/cytoskeleton	1004	55
D51695	TUBB	tubulin, beta polypeptide	cell adhesion/cytoskeleton	295	55
X72460	RPL3	ribosomal protein L3	RNA/protein processing	235	55
U06254	PPP2R1B	protein phosphatase 2 (form 2A), regulatory subunit A (PR65), beta isoform	tumor associated	221	55
U0511561	SLC29A1	solute carrier family 29 (nucleoside transporters), member 1	tumor associated	429	55
A0291505	PICP-C1	p53-induced protein PICP-C1	unknown	259	55

Fig. 2/2

## Cluster A

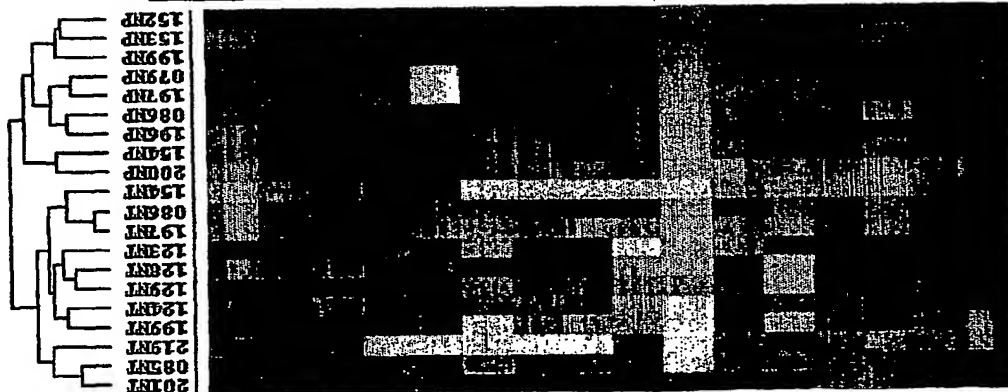


ACCESSION No.	GENE	DESCRIPTION	FUNCTION
AA030866	PC4	activated RNA polymerase II transcription cofactor 4	RNA/protein processing
AA412510		ESTs	unknown
DD50063	PSMD7	proteasome (prosome, macropain) 26S subunit, non-ATPase, 7	bioenergetics
AA806223	TFRC	transferrin receptor (p90, CD71)	
MF29536	EIF2S2	eukaryotic translation initiation factor 2, subunit 2 (beta, 38kD)	RNA/protein processing
AA742444	HSPA8	heat shock 70kD protein 8	RNA/protein processing
XS2882	TCP1	t-complex 1	RNA/protein processing
U03464	COL1A2	collagen, type I, alpha 2	cell adhesion / cytoskeleton
AA308436	C20ORF3	chromosome 20open reading frame 3	unknown
MB1601	TCEA1	transcription elongation factor A (SII), 1	RNA/protein processing
U03250	TOP1	topoisomerase (DNA) I	
X02152	LDHA	lactate dehydrogenase A	bioenergetics
AA042906	PSMB8	proteasome (prosome, macropain) subunit, beta type, 8	bioenergetics
V00572	PGK1	phosphoglycerate kinase 1	bioenergetics
V00572	PGK1	phosphoglycerate kinase 1	bioenergetics
X02152	LDHA	lactate dehydrogenase A	bioenergetics
N39356	PGK1	phosphoglycerate kinase 1	bioenergetics
AA364124	HTATSF1	HIV TAT specific factor 1	RNA/protein processing
A1299952	LOC51765	serine/threonine protein kinase MASK	unknown
AA179452	APBP1	amyloid beta precursor protein-binding protein 1, 59kD	unknown
AA904688	PRO2463	PRO2463 protein	unknown
AA031669	VDAC3	voltage-dependent anion channel 3	bioenergetics
AF038962	VDAC3	voltage-dependent anion channel 3	bioenergetics
U34683	GSS	glutathione synthetase	bioenergetics

Fig. 3

3 / 1 / 6

# Cluster B



ACCESSION No.	GENE	DESCRIPTION	FUNCTION
Y53463	GPX2	glutathione peroxidase 2 (gastrointestinal)	bioenergetics
AA502642	PP1A	peptidylprolyl isomerase A (cyclophilin A)	bioenergetics
L09235	ATP6A1	ATPase, H <sup>+</sup> transporting, lysosomal (vacuolar proton pump), alpha polypeptide	bioenergetics
M33197	GAPD	glyceraldehyde-3-phosphate dehydrogenase	bioenergetics
X70049	DDX1	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 1	cell growth
X03747	ATP1B1	ATPase, Na <sup>+</sup> /K <sup>+</sup> transporting beta 1 polypeptide	bioenergetics
X03747	ATP1B1	ATPase, Na <sup>+</sup> /K <sup>+</sup> transporting beta 1 polypeptide	bioenergetics
AA421248		Homo sapiens P1725 mRNA, complete cds	unknown
AF040260	GMD5	GDP-mannose 4,6-dehydratase	bioenergetics
AA316525		ESTs, Weakly similar to LITB HUMAN LITHOSTATHINE 1 BETA PRECURSOR	unknown
L42176	FHL2	four and a half LIM domains 2	signal transduction
AA346311	RAI3	retinoic acid induced 3	signal transduction
Y13620	BCI9	B-cell CLL/lymphoma 9	unknown
AF070616	HPCAL1	hippocalcin-like 1	unknown
A0040592		Homo sapiens cDNA: FLJ22604 fis, clone HSN04630	unknown
AA421681	CAPN4	calpain 4, small subunit (30K)	protease

Fig. 3/1

3 / 2 / 6

Y11354	TAF2C1	TATA box binding protein (TBP)-associated factor, RNA polymerase II, C1, 130kD	RNA/protein processing
M50459	RPS4Y	ribosomal protein S4, Y-linked	RNA/protein processing
AB007510	PRP8	U5 snRNP-specific protein (220 kD), ortholog of <i>S. cerevisiae</i> Prp8p	RNA/protein processing
D14710	ATP5A1	ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1	bioenergetics
K03000	ALDH1	aldehyde dehydrogenase 1, soluble	bioenergetics
D00017	ANXA2	annexin A2	bioenergetics
K03000	ALDH1	aldehyde dehydrogenase 1, soluble	bioenergetics
AA910550	LEFTB	left-right determination, factor B	signal transduction
X53586	ITGA6	integrin, alpha 6	cell adhesion / cytoskeleton
X55543	XBP1	X-box binding protein 1	transcription factor
A1188196	USP22	ubiquitin specific protease 22	unknown
U10121	ADAR	adenosine deaminase, RNA-specific	bioenergetics
L13210	LGALS3BP	lectin, galactoside-binding, soluble, 3 binding protein (galectin 6 binding protein)	immune



Fig. 3/2

4 / 6

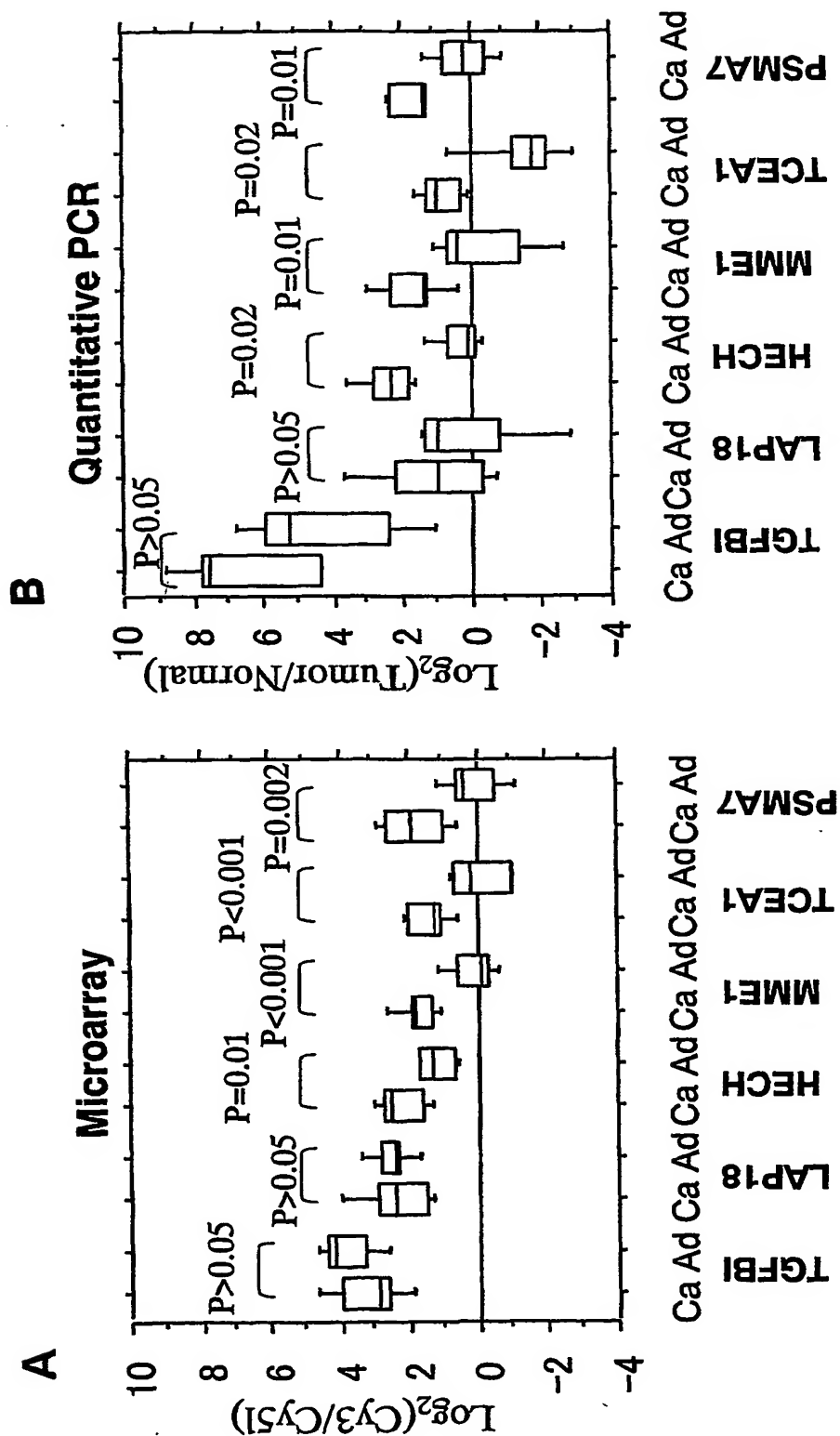
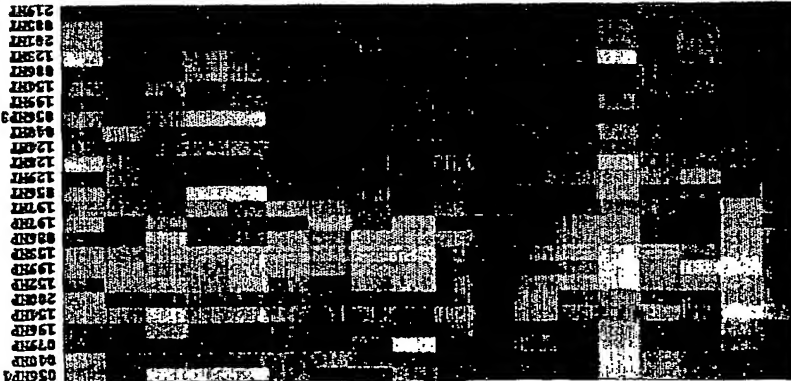
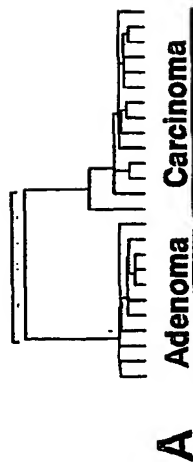


Fig. 4



5 / 6

Fig. 5A



ACCESSION No.	GENE	DESCRIPTION	FUNCTION	P	SIGN
A977821	COL1A1	collagen, type I, alpha 1	cell adhesion/cytoskeleton	<0.001	1
NM_016587	CBX3	chromobox homolog 3	unknown	0.01	1
U20272	GTF3A	general transcription factor IIIA	transcription regulation	0.002	1
J03250	TOP1	topoisomerase (DNA) I	transcription regulation	0.003	1
M81601	TCEA1	transcription elongation factor A (SID), 1	transcription regulation	<0.001	1
X02152	LDHA	lactate dehydrogenase A	bioenergetics	<0.001	1
AA148874	PGAM1	phosphoglycerate mutase 1 (brain)	bioenergetics	<0.001	1
A017668	NDUFS6	NADH dehydrogenase (ubiquinone) Fe-S protein 6	bioenergetics	<0.001	1
X17620	NME1	non-metastatic cells 1, protein (NM23A) expressed in	tumor associated	<0.001	1
U38846	CCT4	chaperonin containing TCP1, subunit 4 (delta)	RNA/protein processing	0.001	1
M94083	CCT6A	chaperonin containing TCP1, subunit 6A (zeta 1)	RNA/protein processing	0.001	1
X52882	TCP1	t-complex 1	RNA/protein processing	<0.001	1
M29536	EIF2S2	eukaryotic translation initiation factor 2, subunit 2	RNA/protein processing	<0.001	1
J03464	COL1A2	collagen, type I, alpha 2	cell adhesion/cytoskeleton	<0.001	1
AA576779	DJ-1	RNA-binding protein regulatory subunit	oncogene	0.001	1
AF022815	PSMA7	proteasome (prosome, macropain) subunit, alpha type, 7	unknown	0.002	1
M61831	AHCY	S-adenosylhomocysteine hydrolase	bioenergetics	0.01	1
U55206	GGH	gamma-glutamyl hydrolase	bioenergetics	0.002	1

5 / 1 / 6

L02326	IGL2	immunoglobulin lambda-like polypeptide 2	immune response	0.01	-1
X55543	XBP1	X-box binding protein 1	transcription regulation	0.004	-1
A1743134	TNRG3	trinucleotide repeat containing 3	unknown	0.002	-1
X53586	ITGA6	integrin, alpha 6	cell adhesion/cytoskeleton	<0.001	-1
U41635	OS-9	amplified in osteosarcoma	tumor associated	<0.001	-1
X04299	ADH3	alcohol dehydrogenase 3 (class I), gamma polypeptide	bioenergetics	0.003	-1
M12963	ADH1	alcohol dehydrogenase 1 (class I), alpha polypeptide	bioenergetics	0.002	-1
M57899	UGT1A1	UDP glucosyltransferase 1 family, polypeptide A1	bioenergetics	<0.001	-1
L15203	TFF3	trefoil factor 3 (intestinal)	unknown	0.001	-1
N34138	GABARAP	GABA(A) receptor-associated protein	unknown	0.002	-1
AF065388	TSPAN1	tetraspan 1	unknown	0.002	-1
L42176	FHL2	four and a half LIM domains 2	signal transduction	<0.001	-1
AA665097	LOC51323	hypothetical protein	unknown	0.001	-1
U60808	GDS1	CDP-diacylglycerol synthase	bioenergetics	0.008	-1
AA447849	SPUVE	protease, serine, 23	unknown	0.01	-1
AA226073	ITIH2C	integral membrane protein 2C	unknown	<0.001	-1
A167917	KIAA0826	KIAA0826 protein	unknown	<0.001	-1
AA443786	FLJ20163	hypothetical protein FLJ20163	unknown	<0.001	-1
AA532514	ESTs	ESTs	unknown	<0.001	-1
AA327452	MUC2	mucin 2, intestinal/tracheal	cell adhesion/cytoskeleton	<0.001	-1
AA573905	FCGBP	Fc fragment of IgG binding protein	immune response	<0.001	-1
AA393152	KIF13B	kinesin 13B	unknown	<0.001	-1
A1338165	HEF1	enhancer of filamentation 1	signal transduction	<0.001	-1
Y00815	PTPRF	protein tyrosine phosphatase, receptor type, F	signal transduction	<0.001	-1
AU149434	RBMX	RNA binding motif protein, X chromosome	RNA/protein processing	<0.001	-1
AA531016	ESTs	ESTs	unknown	0.001	-1
A1190293	TIF1B	KRAB-associated protein 1	transcription regulation	0.01	-1
AA256650	HNA11	beta, 4 mannosyltransferase	bioenergetics	<0.001	-1
AF038440	PLD2	phospholipase D2	bioenergetics	<0.001	-1
A1340150	SOSTM1	sequestosome 1	unknown	0.005	-1
D13900	ECHS1	enoyl Coenzyme A hydratase, short chain, 1	bioenergetics	0.003	-1
AA910550	LEFTB	left-right determination, factor B	signal transduction	0.005	-1

Fig. 5A/1

6 / 6

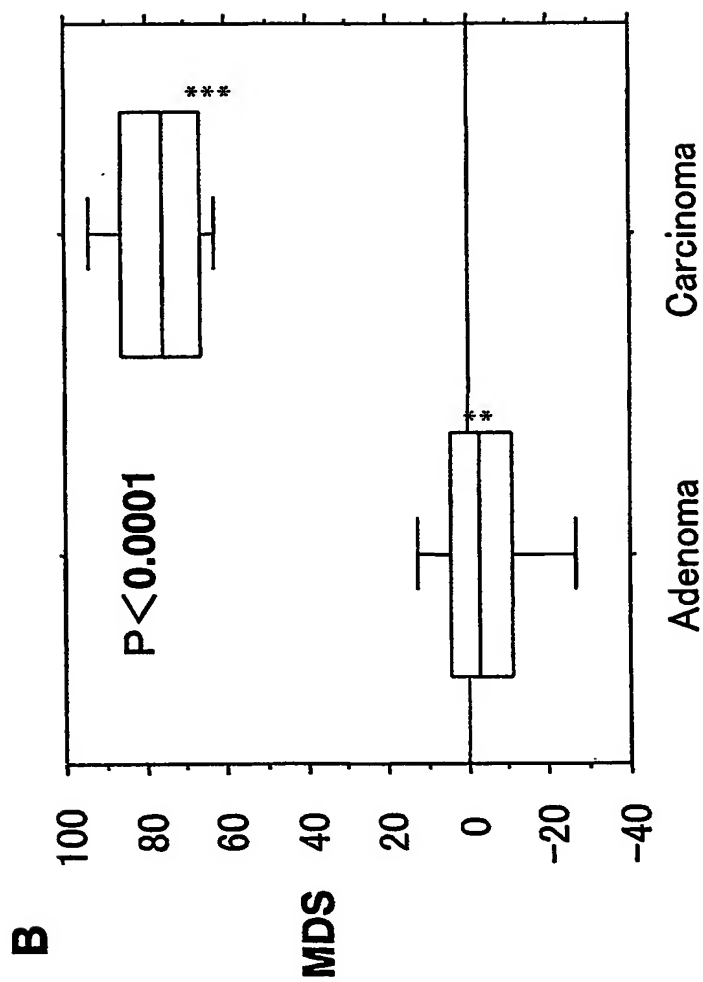


Fig. 5B

**This Page is Inserted by IFW Indexing and Scanning  
Operations and is not part of the Official Record.**

**BEST AVAILABLE IMAGES**

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images include but are not limited to the items checked:

- ☐ **BLACK BORDERS**
- ☐ **IMAGE CUT OFF AT TOP, BOTTOM OR SIDES**
- ☒ **FADED TEXT OR DRAWING**
- ☒ **BLURRED OR ILLEGIBLE TEXT OR DRAWING**
- ☐ **SKEWED/SLANTED IMAGES**
- ☐ **COLOR OR BLACK AND WHITE PHOTOGRAPHS**
- ☐ **GRAY SCALE DOCUMENTS**
- ☐ **LINES OR MARKS ON ORIGINAL DOCUMENT**
- ☐ **REFERENCE(S) OR EXHIBIT(S) SUBMITTED ARE POOR QUALITY**
- ☐ **OTHER:** \_\_\_\_\_

**IMAGES ARE BEST AVAILABLE COPY.**

**As rescanning these documents will not correct the image problems checked, please do not report these problems to the IFW Image Problem Mailbox.**